

36063.32 Da. The predicted domains of the BM-HABP polypeptide are: an HA binding motif domain (amino acid residues Q-121 to L-215 of SEQ ID NO:11), double underlined.

Figures 5A-G show the regions of identity between the amino acid sequence of the full-length WF-HABP protein (SEQ ID NO:2) and the translation product of the human TSG-6 protein (SEQ ID NO:3; See Genbank Accession No. gi|339994), as determined by Megalign (DNA Star suite of programs) analysis. Identical amino acids between the two polypeptides are shaded, while the non-identical regions remain unshaded. By examining the regions of amino acids shaded and/or unshaded, the skilled artisan can readily identify conserved domains between the two polypeptides.

B1
Cont

Figures 6A-B show the regions of identity between the amino acid sequence of the WF-HABP protein (SEQ ID NO:5) and the translation product of the human TSG-6 protein (SEQ ID NO:3; See Genbank Accession No. gi|339994), as determined by Megalign (DNA Star suite of programs) analysis. Identical amino acids between the two polypeptides are shaded, while the non-identical regions remain unshaded. By examining the regions of amino acids shaded and/or unshaded, the skilled artisan can readily identify conserved domains between the two polypeptides.

Figure 7 shows the regions of identity between the amino acid sequence of the OE-HABP protein (SEQ ID NO:8) and the translation product of the Cartilage Link Protein from Gallus gallus (SEQ ID NO:9; See Genbank Accession No. gi|212260), as determined by Megalign (DNA Star suite of programs) analysis. Identical amino acids between the two polypeptides are shaded, while the non-identical regions remain unshaded. By examining the regions of amino acids shaded and/or unshaded, the skilled artisan can readily identify conserved domains between the two polypeptides.

B1
Come

Figure 8 shows the regions of identity between the amino acid sequence of the BM-HABP protein (SEQ ID NO:11) and the translation product of the TSG-6 protein from *Mus musculus* (SEQ ID NO:12; See Genbank Accession No. 2062475), as determined by Megalign (DNA Star suite of programs) analysis. Identical amino acids between the two polypeptides are shaded, while the non-identical regions remain unshaded. By examining the regions of amino acids shaded and/or unshaded, the skilled artisan can readily identify conserved domains between the two polypeptides.

Please amend the paragraphs from page 15, line 17 to page 16, line 15 as follows:

p2

The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding a full-length WF-HABP polypeptide (Figures 1A-H (SEQ ID NO:2)). The full-length WF-HABP protein shown in Figures 1A-H (SEQ ID NO:2) shares sequence homology with the human TSG-6 protein (Figures 5A-G (SEQ ID NO:3)).

The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding a WF-HABP polypeptide (Figures 2A-B (SEQ ID NO:5)), the amino acid sequence of which was determined by sequencing a cloned cDNA (Clone HWFBG79). The WF-HABP protein shown in Figures 2A-B (SEQ ID NO:5) shares sequence homology with human cartilage link protein (Figure 6 (SEQ ID NO:6)). The nucleotide sequence shown in Figures 2A-B (SEQ ID NO:4) was obtained by sequencing a cDNA clone (Clone HWFBG79). On December 1, 1998, the plasmid corresponding to this clone was deposited with the American Type Culture Collection, 10801 University Blvd, Manassas, Virginia, 20110-2209, and was assigned accession number 203503. The deposited cDNA is contained in the pBluescript plasmid (Stratagene, La Jolla, CA).

32 Cont

The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding a OE-HABP polypeptide (Figures 3A-B (SEQ ID NO:8)), the amino acid sequence of which was determined by sequencing a cloned cDNA (Clone HOEDH76). The OE-HABP protein shown in Figures 3A-B (SEQ ID NO:8) shares sequence homology with the Gallus gallus cartilage link protein (Figure 7 (SEQ ID NO:9)). The nucleotide sequence shown in Figures 3A-B (SEQ ID NO:7) was obtained by sequencing a cDNA clone (Clone HOEDH76). On December 1, 1998, the plasmid corresponding to this clone was deposited with the American Type Culture Collection, 10801 University Blvd, Manassas, Virginia, 20110-2209, and was assigned accession number 203501. The deposited cDNA is contained in the pBluescript plasmid (Stratagene, La Jolla, CA).

The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding a BM-HABP polypeptide (Figures 4A-B (SEQ ID NO:11)), the amino acid sequence of which was determined by sequencing a cloned cDNA (Clone HB MVC21). The BM-HABP protein shown in Figures 4A-B (SEQ ID NO:11) shares sequence homology with the Mus musculus TSG-6 protein (Figure 8 (SEQ ID NO:12)). The nucleotide sequence shown in Figures 4A-B (SEQ ID NO:10) was obtained by sequencing a cDNA clone (Clone HB MVC21). On December 1, 1998, the plasmid corresponding to this clone was deposited with the American Type Culture Collection, 10801 University Blvd, Manassas, Virginia, 20110-2209, and was assigned accession number 203502. The deposited cDNA is contained in the pBluescript plasmid (Stratagene, La Jolla, CA).

Please amend the paragraphs from page 19, line 16 to page 20, line 33 as follows:

The determined nucleotide sequence of the full-length WF-HABP cDNA of

63
Figures 1A-H (SEQ ID NO:1) contains an open reading frame encoding a polytopic polypeptide of about 2100 amino acid residues, with a HA-binding domain, EGF-like Type 1 domains, EGF-like Type 2 domains; laminin-type EGF domains; link protein domain; cytochrome P450 cysteine heme-iron ligand binding domains; a prokaryotic membrane lipoprotein lipid attachment site domains, and having a deduced molecular weight of about 231445.37 Da. The WF-HABP protein shown in Figures 1A-H (SEQ ID NO:2) is predicted to contain domains which are about 48% identical to the human hyaluronan binding protein TSG-6 protein depicted in SEQ ID NO:6 (see Figures 5A-G) using the computer program "MegAlign" (DNASTAR suite of software programs). In addition to having homology, TSG-6 and the full-length WF-HABP are thought to share the same topological structure based upon their intrinsic hyaluronan binding activity. For example, like TSG-6, the full-length WF-HABP contains a hyaluronan binding domain. As discussed above, TSG-6 has been shown to be a hyaluronan binding protein and play a vital role in arthritis, antiinflammatory activity, and the vascular injury response.

The determined nucleotide sequence of the WF-HABP cDNA of Figures 2A-B (SEQ ID NO:4) contains an open reading frame encoding a polytopic polypeptide of about 457 amino acid residues, with a HA-binding domain, an EGF-like Type 2 domain, and a link protein domain, and having a deduced molecular weight of about 48448.90 Da. The WF-HABP protein shown in Figures 2A-B (SEQ ID NO:5) is predicted to be about 48% identical to the human hyaluronan binding protein TSG-6 protein depicted in SEQ ID NO:6 (see Figure 6) using the computer program "MegAlign" (DNASTAR suite of software programs). In addition to having homology, TSG-6 and WF-HABP are thought to share

the same topological structure based upon their intrinsic hyaluronan binding activity. For example, like TSG-6, WF-HABP contains a hyaluronan binding domain. As discussed above, TSG-6 has been shown to be a hyaluronan binding protein and play a vital role in arthritis, antiinflammatory activity, and the vascular injury response.

B3
Cont

The determined nucleotide sequence of the OE-HABP cDNA of Figures 3A-B (SEQ ID NO:7) contains an open reading frame encoding a polytopic polypeptide of about 289 amino acid residues, with a HA-binding domain, 6 transmembrane domains, 4 extracellular domains, and a pore loop, and having a deduced molecular weight of about 33174.55 Da. The OE-HABP protein shown in Figures 3A-B (SEQ ID NO:8) is predicted to be about 49% identical to the collagen link protein depicted in SEQ ID NO:9 (see Figure 7) using the computer program "MegAlign" (DNASTAR suite of software programs). In addition to having homology, collagen link protein and OE-HABP are thought to share the same topological structure based upon their intrinsic hyaluronan binding activity. For example, like collagen link protein, OE-HABP contains a hyaluronan binding domain. As discussed above, collagen link protein has been shown to be a hyaluronan binding protein and play a vital role in arthritis, antiinflammatory activity, and the vascular injury response.

The determined nucleotide sequence of the BM-HABP cDNA of Figures 4A-B (SEQ ID NO:10) contains an open reading frame encoding a polytopic polypeptide of about 353 amino acid residues, with a HA-binding domain, 6 transmembrane domains, 4 extracellular domains, and a pore loop, and having a deduced molecular weight of about 36063.32 Da. The BM-HABP protein shown in Figures 4A-B (SEQ ID NO:11) is predicted to be about 43% identical to the TSG-6 protein depicted in SEQ ID NO:12 (see Figure 8) using the computer program "MegAlign" (DNASTAR suite of software programs).

B3
Conel

In addition to having homology, the TSG-6 protein and BM-HABP are thought to share the same topological structure based upon their intrinsic hyaluronan binding activity. For example, like the TSG-6 protein, BM-HABP contains a hyaluronan binding domain. As discussed above, TSG-6 protein has been shown to be a hyaluronan binding protein and play a vital role in arthritis, antiinflammatory activity, and the vascular injury response.
